

First Inventor: Robert M. HOFER, et al.

Application No.: 09/759,990

Docket No.: 31276-20026.00

Sheet 1 of 8

1/8

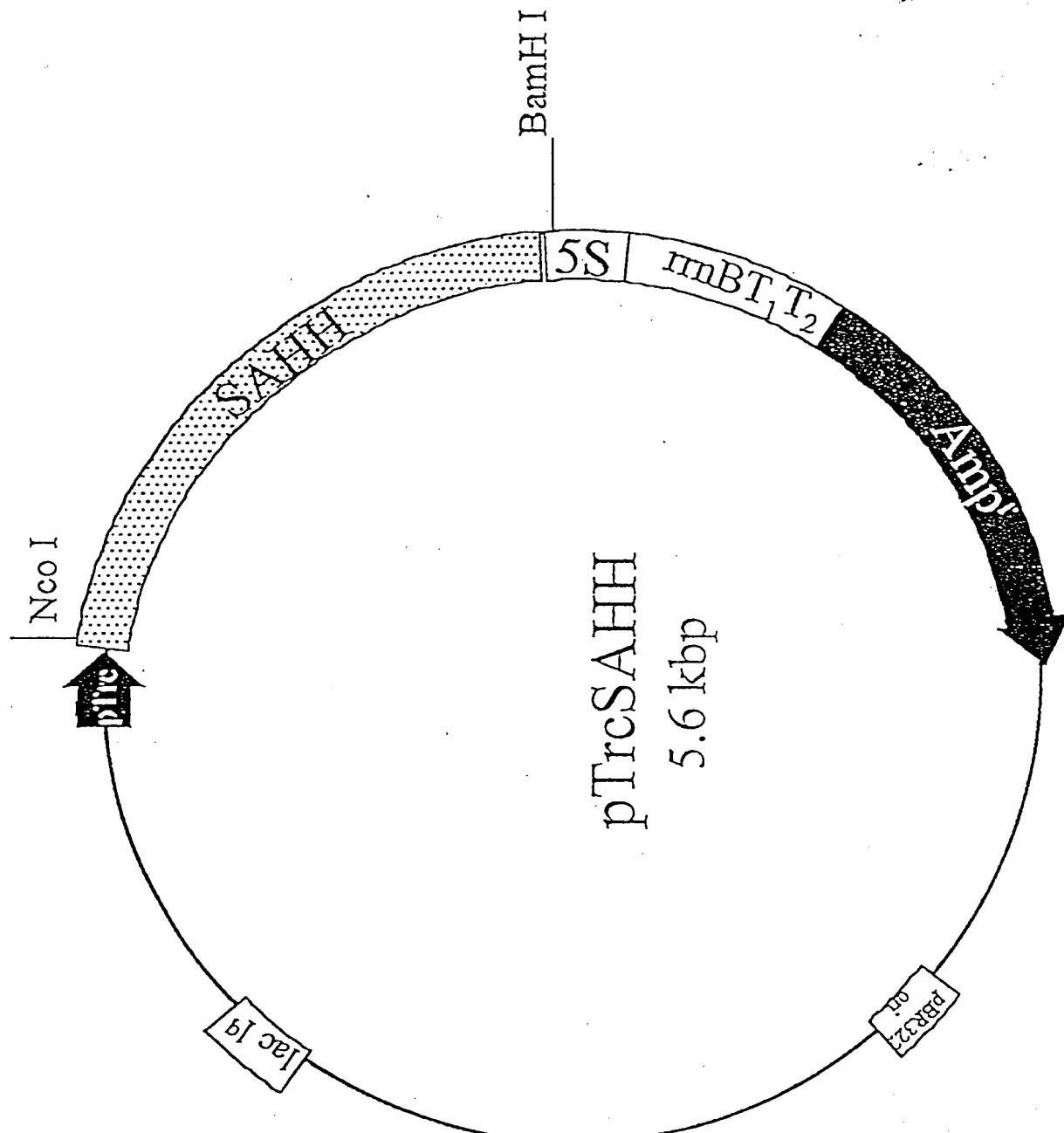


Figure 1

# Stability Study of SAHH

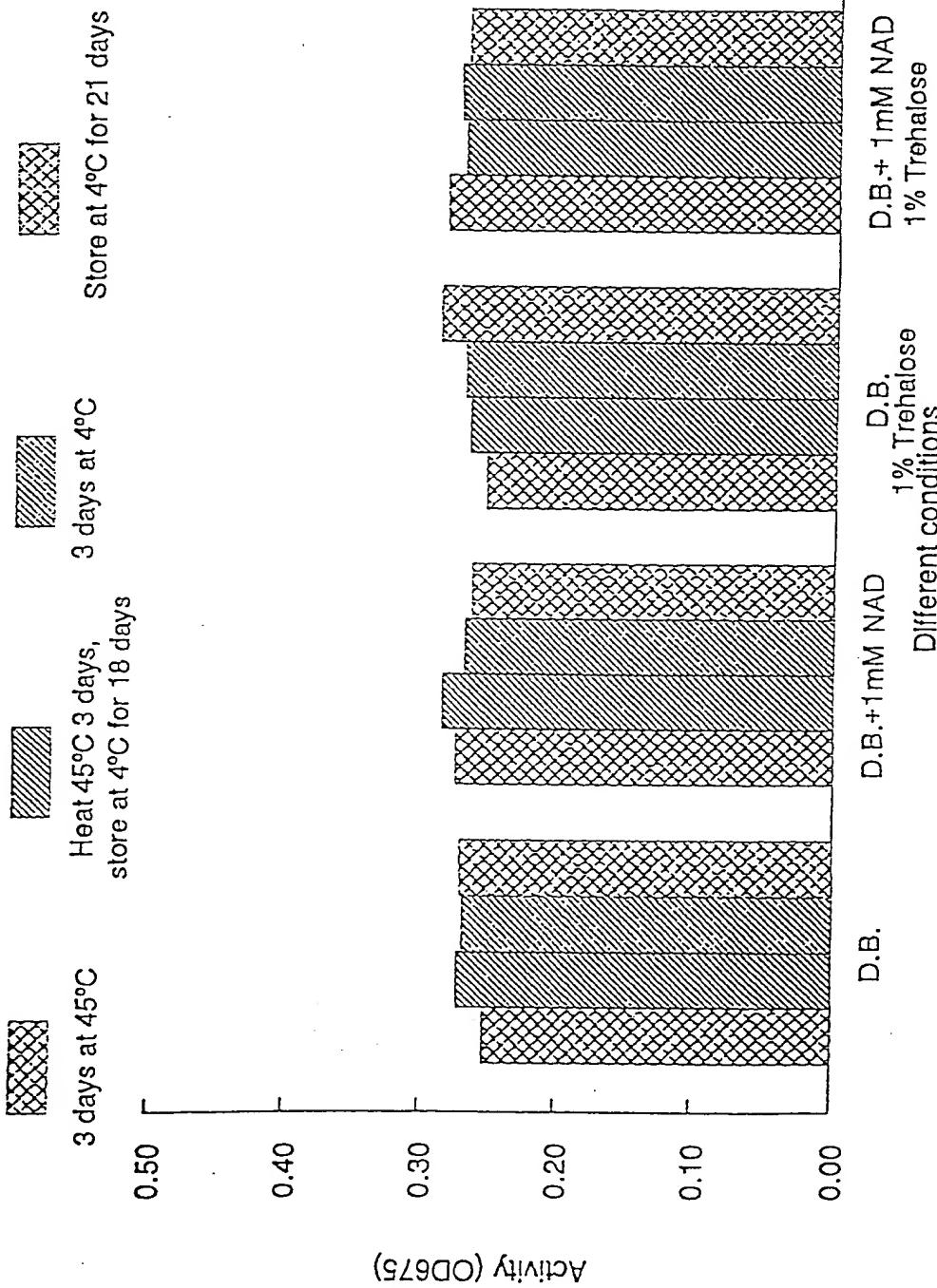


Figure 2

Title: HIGH EXPRESSION AND PRODUCTION OF HIGH-SPECIFIC ACTIVITY RECOMBINANT S-ADENOSYL HOMOCYSTEINASE (SAHH) AND IMPROVED ASSAY FOR S-ADENOSYLMETHIONINE (SAM)  
First Inventor: Robert M. HORN et al.  
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Sheet 2 of 8  
2/8

# Screening of SAHH

Title: HIGH EXPRESSION AND PRODUCTION OF HIGH-SPECIFIC ACTIVITY RECOMBINANT S-ADENOSYL HOMOCYSTEINASE (SAHH) AND IMPROVED ASSAY FOR S-ADENOSYLMETHIONINE (SAM)  
First Inventor: Robert M. ROSENSTEIN, et al.  
Application No.: 09/759,990  
Docket No.: 31276-20026.00  
Sheet 3 of 8

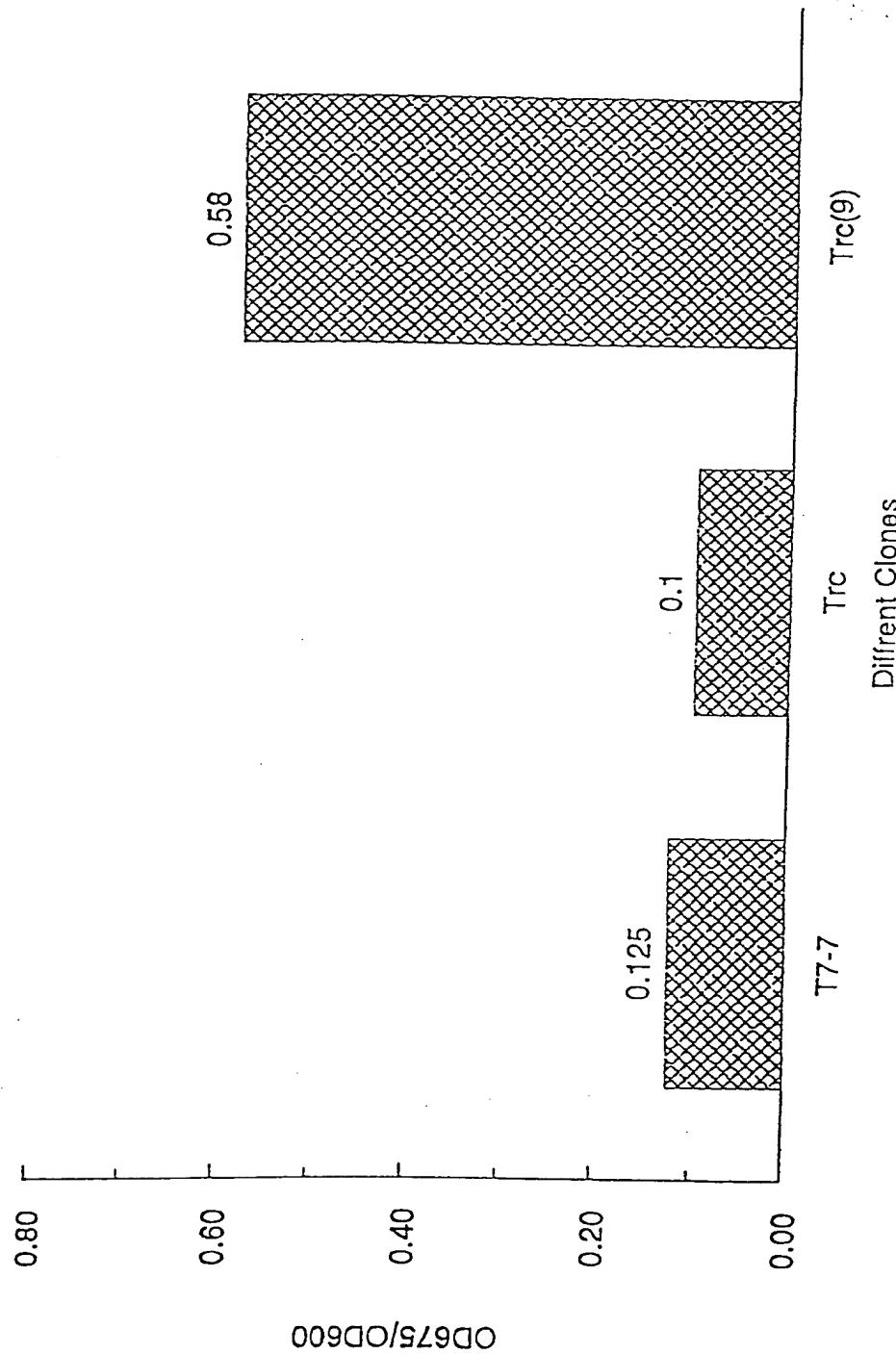


Figure 3

4/8

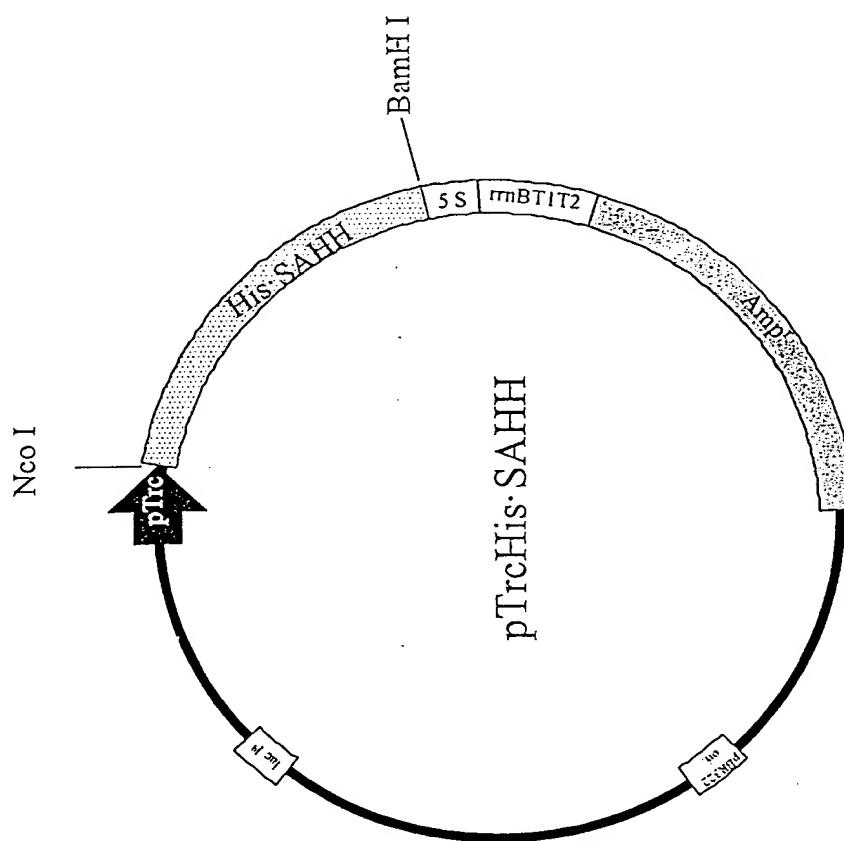


Figure 4

5/8

Stability of SAHH.His

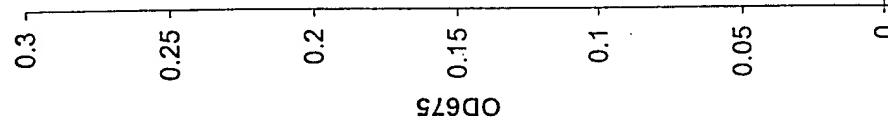


Figure 5

99.2% identity in 1461 residues overlap; Score: 1437.0; Gap frequency: 0.0%

SAHH-wild	291	ATGGCTTCAAATCACCTGCTGGTGTCCATTGAGTACAGAATTGCCGACATCAACCTC
A/C,	71	ATGGCTTCAAATCACCTACTGGTGTCCATTGAGTACAGAATTGCCGACATCAACCTC
		*****
SAHH-wild	351	CATGTTCTCGGCCGTAAAGGAACCTACCCCTGCTGAGAAGGAAATGCCAGGTCTTATGGTT
A/C,	131	CATGTTCTCGGCCGTAAAGGAACCTACCCCTGCTGAGAAGGAAATGCCAGGTCTTATGGTT
		*****
SAHH-wild	411	CTTCGTGAGCGTTATTCCGCTTCTAACGCATTGAAGGGTGTCAAGAATCTCTGGTCCCTC
A/C,	191	CTTCGTGAGCGTTATTCCGCTTCTAACGCATTGAAGGGTGTCAAGAATCTCTGGTCCCTC
		*****
SAHH-wild	471	CACATGACAGTCCAGACAGCGGTCTTATTGAGACACTCACAGCTTGGTGTGATGTC
A/C,	251	CACATGACAGTCCAGACAGCGGTCTCATCGAGACACTCACAGCTTGGTGTGATGTC
		*****
SAHH-wild	531	AGATGGGCTCCTGCAACATCTCTACACAAGATAACAGCCGTGCTGCTATCGTTGTC
A/C,	311	AGATGGGCTCCTGCAACATCTCTACACAAGATAACAGCCGTGCTGCTATCGTTGTC
		*****
SAHH-wild	591	GGCCAACAGGCACACCAGAGAAGCCAGGCCGGTATCCCAGTCTTCGCCTGGAAGGGCGAA
A/C,	371	GGCCAACAGGCACACCAGAGAAGCCAGGCCGGTATCCCAGTCTTCGCCTGGAAGGGCGAA
		*****
SAHH-wild	651	ACACTCCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGGCCAGATGGTCAAGGC
A/C,	431	ACACTCCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGGCCAGATGGTCAAGGC
		*****
SAHH-wild	711	CCACAGCAGGTTGTCGATGATGGTGGTGTACACTCCTCATCTCCAAGGGCTTCGAA
A/C,	491	CCACAGCAGGTTGTCGATGATGGTGGTGTACACTCCTCATCTCCAAGGGCTTCGAA
		*****
SAHH-wild	771	TTCGAAACAGCCGGTGTCTCCAGAGCCAACAGAGCTGACAAACCTCGAATACCGCTGC
A/C,	551	TTCGAAACAGCCGGTGTCTCCAGAGCCAACAGAGCTGACAAACCTCGAATACCGCTGC
		*****
SAHH-wild	831	GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGAACAAACCACAGTTGCT
A/C,	611	GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGAACAAACCACAGTTGCT
		*****
SAHH-wild	891	GCCGGCATGAACGGTCTTCCGAAGAGACAACAACAGGTGTCCACCGCCTTACCGCTC
A/C,	671	GCCGGCATGAACGGTCTTCCGAAGAGACAACAACAGGTGTCCACCGCCTTACCGCTC
		*****
SAHH-wild	951	GAGAAGGAGGGCAAACCTCTTCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC
A/C,	731	GAGAAGGAGGGCAAACCTCTTCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC
		*****
SAHH-wild	1011	AAGTCGATAACATCTACGGCTGCGCACTCCATTACGATGGTATCAACCGTCTTCC
A/C,	791	AAGTCGATAACATCTACGGCTGCGCACTCCATTACGATGGTATCAACCGTCTTCC
		*****
SAHH-wild	1071	GATGTCATGATGGCGCAAGACAGCTCTCGTCATGGTTACGGCATGTCGGAGGGC
A/C,	851	GATGTCATGATGGCGCAAGACAGCTCTCGTCATGGTTACGGCATGTCGGAGGGC
		*****
SAHH-wild	1131	TCGCTCAATCCCTCCGTGGCCAAGGCGCTCGCTTACATCACAGAAGTCGACCCATAC
A/C,	911	TCGCTCAATCCCTCCGTGGCCAAGGCGCTCGCTTACATCACAGAAGTCGACCCATAC
		*****

Figure 6a

SAHH-wild A/C,	1191	TGCGCTCTCCAGGCTGTACATGGAAGGCTACCAGGTCCGCCGCATCGAGGAAGTCGTCAAG
	971	TGCGCTCTCCAGGCTGCCATGGAAGGCTACCAGGTCCGCCGCATCGAGGAAGTCGTCAAG
		*****
SAHH-wild A/C,	1251	GATGTCGATATCTCGTTACATGCACAGGAAACTGCGATATCATCTCTGTTGACATGATG
	1031	GATGTCGATATCTCGTTACATGCACAGGAAACTGCGATATCATCTCTGTTGACATGATG
		*****
SAHH-wild A/C,	1311	GCCCAGATGAAGGATAAGGCTATTGTCGGTAACATCGGCCACTTCGATAACGAAATTGAT
	1091	GCCCAGATGAAGGATAAGGCTATTGTCGGTAACATCGGCCACTTCGATAACGAAATTGAT
		*****
SAHH-wild A/C,	1371	ACAGATGGCCTCATGAAATACCCAGGCATCAAGCACATCCCAATCAAGCCAGAACAGAC
	1151	ACAGATGGCCTCATGAAATACCCAGGCATCAAGCACATCCCAATCAAGCCAGAACAGAC
		*****
SAHH-wildt A/C,	1431	ATGTGGGAATTCCAGATGGCCACGCTATCCTCCTTCTGCTGAGGGCCGCCCTCTAAC
	1211	ATGTGGGAATTCCAGATGGCCACGCTATCCTCCTTCTGCTGAGGGCCGCCCTCTAAC
		*****
SAHH-wild A/C,	1491	CTTGGTTGCGCTACAGGTACCCATTTCGTTATGTCATGTCATTCAACAAACAGACA
	1271	CTTGGCTGCGCTACAGGTACCCATTTCGTTATGTCATGTCATTCAACAAACAGACA
		*****
SAHH-wild A/C,	1551	CTCGCTCAGCTCGACCTCTACGAAAAGAGAGGAAATCTCGAGATGAAGGTTACACACTT
	1331	CTCGCTCAGCTCGACCTCTACGAAAAGAGAGGAAATCTCGAGAAGAAGGTTACACACTT
		*****
SAHH-wild A/C,	1611	CCGAAGCATCTCGATGAAGAAGTCGTTGCCCTCCACCTCGGATCTCTCGATGTCCACCTT
	1391	CCGAAGCATCTCGATGAAGAAGTCGCTGCCCTCCACCTCGGATCTCTCGATGTCCACCTT
		*****
SAHH-wild A/C,	1671	ACAAAGCTTACACAGAACAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGCCTTACAAG
	1451	ACAAAGCTTACACAGAACAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGCCTTACAAG
		*****
SAHH-wild A/C,	1731	TCTGATGCTTACCGTTATTAA
	1511	TCTGATGCTTACCGTTATTAA
		*****

65.9% identity in 44 residues overlap; Score: 14.0; Gap frequency: 0.0%

80.0% identity in 20 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 1053 GGTATCAACCGTGTCCGA  
A/C, 674 GGCAATGAACGGTGTCCGA  
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**Figure 6b**

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87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 564 GATAACAGCCGCTGCTG  
A/C, 554 GAAACAGCCGGTGCTG  
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64.3% identity in 42 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 1224 GTCCCGCCGCATCGAGGAAGTCGTCAAGGATGTCGATATCTTC  
A/C, 710 GTCCACCGCCTCTACCAGCTCGAGAAGGAGGGCAAACCTCCTC  
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87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 774 GAAACAGCCGGTGCTG  
A/C, 344 GATAACAGCCGCTGCTG  
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Figure 6c